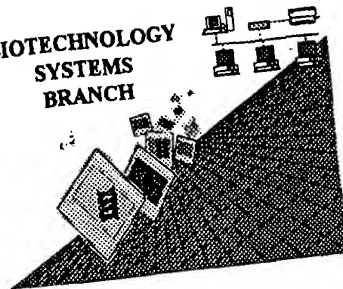


RAW SEQUENCE LISTING ERROR REPORT

BIOTECHNOLOGY
SYSTEMS
BRANCH



0590
1212

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/992,600

Source: OIP

Date Processed by STIC: 12/5/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
 - 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
- FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER
VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND
TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25. Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
<http://www.uspto.gov/web/offices/pac/checker>

OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/992,600

DATE: 12/05/2001

TIME: 12:20:09

Input Set : D:\Seqlist.txt

Output Set: N:\CRF3\11212001\I992600.raw

Does Not Comply

Corrected Diskette Needed

nr 2-3

OK>

3 <110> APPLICANT: Benjanin, Stephane
 4 Tanaka, Hiroaki
 6 <120> TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
 8 <130> FILE REFERENCE: 91.US4.DIV
 10 <140> CURRENT APPLICATION NUMBER: US/09/992,600
 11 <141> CURRENT FILING DATE: 2001-11-13
 13 <150> PRIOR APPLICATION NUMBER: US 09/924,340
 14 <151> PRIOR FILING DATE: 2001-08-06
 16 <150> PRIOR APPLICATION NUMBER: PCT/IB01/01715
 17 <151> PRIOR FILING DATE: 2001-08-06
 19 <150> PRIOR APPLICATION NUMBER: US 60/305,456
 20 <151> PRIOR FILING DATE: 2001-07-13
 22 <150> PRIOR APPLICATION NUMBER: US 60/302,277
 23 <151> PRIOR FILING DATE: 2001-06-29
 25 <150> PRIOR APPLICATION NUMBER: US 60/298,698
 26 <151> PRIOR FILING DATE: 2001-06-15
 28 <150> PRIOR APPLICATION NUMBER: US 60/293,574
 29 <151> PRIOR FILING DATE: 2001-05-25
 31 <160> NUMBER OF SEQ ID NOS: 112
 33 <170> SOFTWARE: JPatent

ERRORED SEQUENCES

6602 <210> SEQ ID NO: 112
 6603 <211> LENGTH: 387
 6604 <212> TYPE: PRT
 6605 <213> ORGANISM: Homo sapiens
 6607 <400> SEQUENCE: 112
 6608 Met Ser Thr Phe Phe Ser Asp Thr Ala Trp Ile Cys Leu Ala Val Pro
 6609 1 5 10 15
 6610 Thr Val Leu Cys Gly Thr Val Phe Cys Lys Tyr Lys Lys Ser Ser Gly
 6611 20 25 30
 6612 Gln Leu Trp Ser Trp Met Val Cys Leu Ala Gly Leu Cys Ala Val Cys
 6613 35 40 45
 6614 Leu Leu Ile Leu Ser Pro Phe Trp Gly Leu Ile Leu Phe Ser Val Ser
 6615 50 55 60
 6616 Cys Phe Leu Met Tyr Thr Tyr Leu Ser Gly Gln Glu Leu Leu Pro Val
 6617 65 70 75 80
 6618 Asp Gln Lys Ala Val Leu Val Thr Gly Gly Asp Cys Gly Leu Gly His
 6619 85 90 95
 6620 Ala Leu Cys Lys Tyr Leu Asp Glu Leu Gly Phe Thr Val Phe Ala Gly
 6621 100 105 110
 6622 Val Leu Asn Glu Asn Gly Pro Gly Ala Glu Glu Leu Arg Arg Thr Cys
 6623 115 120 125
 6624 Ser Pro Arg Leu Ser Val Leu Gln Met Asp Ile Thr Lys Pro Val Gln
 6625 130 135 140

P. 2

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/992,600

DATE: 12/05/2001

TIME: 12:20:11

Input Set : D:\Seqlist.txt

Output Set: N:\CRF3\11212001\I992600.raw

```

6626 Ile Lys Asp Ala Tyr Ser Lys Val Ala Ala Met Leu Gln Asp Arg Gly
6627 145 150 155 160
6628 Leu Trp Ala Val Ile Asn Asn Ala Gly Val Leu Gly Phe Pro Thr Asp
6629 165 170 175
6630 Gly Glu Leu Leu Leu Met Thr Asp Tyr Lys Gln Cys Met Ala Val Asn
6631 180 185 190
6632 Phe Phe Gly Thr Val Glu Val Thr Lys Thr Phe Leu Pro Leu Leu Arg
6633 195 200 205
6634 Lys Ser Lys Gly Arg Leu Val Asn Val Ser Ser Met Gly Gly Gly Ala
6635 210 215 220
6636 Pro Val Glu Arg Leu Ala Ser Tyr Gly Ser Ser Lys Ala Ala Val Thr
6637 225 230 235 240
6638 Met Phe Ser Ser Val Met Arg Leu Glu Leu Ser Lys Trp Gly Ile Lys
6639 245 250 255
6640 Val Ala Ser Ile Gln Pro Gly Gly Phe Leu Thr Asn Ile Ala Gly Thr
6641 260 265 270
6642 Ser Asp Lys Trp Glu Lys Leu Glu Lys Asp Ile Leu Asp His Leu Pro
6643 275 280 285
6644 Ala Glu Val Gln Glu Asp Tyr Cys Gln Asp Tyr Ile Leu Ala Gln Arg
6645 290 295 300
6646 Asn Phe Leu Leu Leu Ile Asn Ser Leu Ala Ser Lys Asp Phe Ser Pro
6647 305 310 315 320
6648 Val Leu Arg Asp Ile Gln His Ala Ile Leu Ala Lys Ser Pro Phe Ala
6649 325 330 335
6650 Tyr Tyr Thr Pro Gly Lys Gly Ala Tyr Leu Trp Ile Cys Leu Ala His
6651 340 345 350
6652 Tyr Leu Pro Ile Gly Ile Tyr Asp Tyr Phe Ala Lys Arg His Phe Gly
6653 355 360 365
6654 Gln Asp Lys Pro Met Pro Arg Ala Leu Arg Met Pro Asn Tyr Lys Lys
6655 370 375 380
6656 Lys Ala Pro
6657 385

```

E-->

6658 (1) delete at end of file

see next page for more errors

Use of n and/or Xaa has been detected in the Sequence Listing.
 Review the Sequence Listing to insure a corresponding
 explanation is presented in the <220> to <223> fields of
 each sequence using n or Xaa.

<210> 30
 <211> 258
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> 1..20

<220>

<221> UNSURE

<222> (49) 29 ←

<223> Xaa = Glu, (*)

<400> 30

Met Gly Arg Thr Arg Glu Ala Gly Cys Val Ala Ala Gly Val Val Ile
 -20 -15 -10 -5
 Gly Ala Gly Ala Cys Tyr Cys Val Tyr Arg Leu Ala Trp Gly Arg Asp
 1 5 10
 Glu Asn Glu Lys Ile Trp Asp Glu Asp Glu Glu Ser Thr Asp Thr Ser
 15 20 25
 (Xaa) Ile Gly Val Glu Thr Val Lys Gly Ala Lys Thr Asn Ala Gly Ala
 30 35 40
 Gly Ser Gly Ala Lys Leu Gln Gly Asp Ser Glu Val Lys Pro Glu Val
 45 50 55 60
 Ser Leu Gly Leu Glu Asp Cys Pro Gly Val Lys Glu Lys Ala His Ser
 65 70 75
 Gly Ser His Ser Gly Gly Gly Leu Glu Ala Lys Ala Lys Ala Leu Phe
 80 85 90
 Asn Thr Leu Lys Glu Gln Ala Ser Ala Lys Ala Gly Lys Gly Ala Arg
 95 100 105
 Val Gly Thr Ile Ser Gly Asn Arg Thr Leu Ala Pro Ser Leu Pro Cys
 110 115 120
 Pro Gly Gly Arg Gly Gly Gly Cys His Pro Thr Arg Ser Gly Ser Arg
 125 130 135 140
 Ala Gly Gly Arg Ala Ser Gly Lys Ser Lys Gly Lys Ala Arg Ser Lys
 145 150 155
 Ser Thr Arg Ala Pro Ala Thr Thr Trp Pro Val Arg Arg Gly Lys Phe
 160 165 170
 Asn Phe Pro Tyr Lys Ile Asp Asp Ile Leu Ser Ala Pro Asp Leu Gln
 175 180 185
 Lys Val Leu Asn Ile Leu Glu Arg Thr Asn Asp Pro Phe Ile Gln Glu
 190 195 200
 Val Ala Leu Val Thr Leu Gly Asn Asn Ala Ala Tyr Ser Phe Asn Gln
 205 210 215 220
 Asn Ala Ile Arg Glu Leu Gly Gly Val Pro Ile Ile Ala Lys Lys Lys
 225 230 235
 Lys Lys

the Xaa is at location 29 (a positive (+) 29)
 Xaa cannot represent a stop codon
 or a gap in the sequence

"49" denotes
 a positive (+)
 49, not the
 49th position
 in the
 sequence,
 when the
 sequence includes
 negative
 numbers

e.g. if the
 Xaa were in
 the second position
 in the sequence, the
 <222>
 Please ^{response} would be
 correct and -19.
 identical error
 in Sequence 72.

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/992,600

DATE: 12/05/2001

TIME: 12:20:12

Input Set : D:\Seqlist.txt

Output Set: N:\CRF3\11212001\I992600.raw

L:10 M:270 C: Current Application Number differs, Replaced Application Number
 L:1477 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:27
 L:1477 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27
 L:1498 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:27
 L:1498 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27
 L:1544 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28
 L:1558 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28
 L:1599 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:29
 L:1599 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:29
 L:1662 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:30
 L:4096 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:71
 L:4096 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:71
 L:4163 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:72
 L:6658 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:112